



SEQUENCE LISTING

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<120> DEPLETION OF ENDOGENOUS PRIMORDIAL GERM CELLS IN AVIAN SPECIES

<130> 297/204 PCT

<150> US 60/440,424

<151> 2003-01-16

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 1989

<212> DNA

<213> Gallus gallus

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<221> CDS

<222> (1)..(1989)

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Ser Gln Gly Arg Ser Glu Glu Gln Ala Trp Met Ala Asn Ser Gly Arg	
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cca aac agc cca tcc ctc cgc ttc tcc agc aga cca agc agc ccc ttg	144
Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu	
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Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln	
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aat aaa ggc tca ctt ggt gct aat gaa gga ctt aac aga agt ctg cct	240
Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro	
65 70 75 80	
gtg cag cat gac att gga gga tat tct ggg agc aga gag tct gtt gta	288
Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val	
85 90 95	
cgt caa aac aga gaa gat caa cca gtg act aga ttt ggt aga ggg agg	336
Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg	
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tgt tat cag tca gga att aat ttt gac aag tat gat gaa tgt gct gtt Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val 210 215 220	672
gag atg tca gga ctt gac cct cca gca cca tta ctg gct ttt gaa gaa Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu 225 230 235 240	720
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tca aaa ctt act cca gtg cag aag cac agc att cct gtt ata caa gca Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala 260 265 270	816
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gct ttt ctt cta cca att gtg gac cgg atg atg aaa gat ggt gta act Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr 290 295 300	912
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act aga gaa ctg ata aat cag atc ttc tta gaa gca agg aag ttt gtg Thr Arg Glu Leu Ile Asn Gln Ile Phe Leu Glu Ala Arg Lys Phe Val 325 330 335	1008

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ggg cat tca atc cgt caa ata atg caa ggc tgt aat ata tta tgt gcc	1104
Gly His Ser Ile Arg Gln Ile Met Gln Gly Cys Asn Ile Leu Cys Ala	
355 360 365	
act cct gga agg ctt ctt gac att att gaa aaa ggg aag atc agt ttg	1152
Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu	
370 375 380	
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Val Glu Val Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp	
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Met Gly Phe Gly Leu Asp Met Lys Lys Leu Ile Ser Tyr Pro Glu Met	
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Pro Ser Lys Asp Arg Arg Gln Thr Leu Met Phe Ser Ala Thr Phe Pro	
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gag gaa gtt caa agg ctg gct ggt gaa ttt ttg aaa acg gac tat ata	1344
Glu Glu Val Gln Arg Leu Ala Gly Glu Phe Leu Lys Thr Asp Tyr Ile	
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Phe Leu Val Ile Gly Asn Thr Cys Gly Ala Cys Ser Asp Val Gln Gln	
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aat att ctt cag gtt ccc cgg tta tcc aag agg gat aaa cta ata gaa	1440
Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu	
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Ile Leu Gln Ser Thr Gly Gly Glu Arg Thr Met Val Phe Val Asp Thr	
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Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu	
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Pro Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg Glu Arg Glu Ile	
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tcg gta gca tca aga ggc ctg gat att gaa aat gtt caa cat gtt att	1680
Ser Val Ala Ser Arg Gly Leu Asp Ile Glu Asn Val Gln His Val Ile	
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Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly	
565 570 575	
cga act ggt cgt tgt gga aat act ggc aaa gca gtt tca ttc ttt gat	1776
Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp	
580 585 590	
gat cag tca gat ggc cat ctt gta caa tca cta ctt aaa gtg ctt tcc	1824
Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser	
595 600 605	
aga acc cag cag gaa ttc cag ttt ggt gga aga atg gct gtc caa aga	1872
Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg	
610 615 620	
aca aat att gtt gct tca act tgg tgc cca aag gga tta atg cag gcc	1920
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625 630 635 640	
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Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro	
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Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val
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Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val
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Thr Tyr Val Pro Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala
195 200 205

Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val
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Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu
225 230 235 240

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260 265 270

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Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr
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Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu
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Glu Glu Val Gln Arg Leu Ala Gly Glu Phe Leu Lys Thr Asp Tyr Ile
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Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu
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Ile Leu Gln Ser Thr Gly Gly Glu Arg Thr Met Val Phe Val Asp Thr
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Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu
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Pro Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg Glu Arg Glu Ile
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595 600 605

Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg
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 His Ser Ser Thr Thr Cys Gln Gly Tyr Val Leu Pro Glu Gly Lys Ile
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 gca gaa att cgg agt tac ttt gaa caa tat ggt act gtg aag gag gtg 368
 Ala Glu Ile Arg Ser Tyr Phe Glu Gln Tyr Gly Thr Val Lys Glu Val
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 aaa ata atc act gac aga act ggt gtt tcc aaa ggg tat gga ttt gtt 416
 Lys Ile Ile Thr Asp Arg Thr Gly Val Ser Lys Gly Tyr Gly Phe Val
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 Pro Ala Pro Gln Phe His Ser Val Trp Thr Asn Gln Asn Thr Glu Thr
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 35 40 45

Glu Ala Glu Ile Arg Ser Tyr Phe Glu Gln Tyr Gly Thr Val Lys Glu
 50 55 60

Val Lys Ile Ile Thr Asp Arg Thr Gly Val Ser Lys Gly Tyr Gly Phe
 65 70 75 80

Val Ser Phe Leu Asp Asn Val Asp Val Gln Lys Ile Val Glu Ser Gln
 85 90 95

Ile Ser Val His Gly Lys Arg Leu Lys Leu Gly Pro Ala Ile Arg Lys
 100 105 110

Gln Gln Asn Leu Cys Ser Tyr Met Gln Pro Arg Pro Leu Ala Phe Asn
 115 120 125

Pro Pro Ala Pro Gln Phe His Ser Val Trp Thr Asn Gln Asn Thr Glu
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Thr Tyr Val Gln Pro Gln Ala Val Val Ser Pro Leu Thr Gln Tyr Val
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Gln Thr Tyr Ala Tyr Ser Ser Pro Ala Val Leu Ile Gln Gln Gln Val
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Pro Val Gly Tyr Gln Pro Ala Tyr Asn Tyr Gln Ala Pro Pro Gln Trp
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Val Pro Gly Glu Gln Arg Asn Tyr Val Met Pro Pro Val Tyr Thr Ser
195 200 205

Val Asn Tyr His Tyr Ser Glu Asp Pro Glu Phe Ile Gln Thr Glu Cys
210 215 220

Ala Val Pro Glu Pro Thr Gln Met Ser Gly Asn Ser Pro Gln Lys Lys
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Ser Val Asp Arg Ser Ile Gln Thr Val Val Ser Cys Leu Phe Asn Pro
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